

GenCore version 5.1.6
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OM protein - protein search, using sw mode!

Run on: December 26, 2004, 16:59:06 ; Search time 12:1928. Seconds
1996.498 Million cell updates/sec

Title: US-10-655-873-8

Perfect score: 1304

Sequence: 1 MWPGGSASOPPPSSAATGL.....HAFIRAVTIDRYMSYLNAS 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 9616763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database : PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	100.0	253	B38957	interleukin 12A precursor [validated] - human interleukin 12A precursor [validated] - human interleukin 12A precursor [validated] - human interleukin 12A precursor [validated]
2	644	49.4	215	2 156135	interleukin 12B p35 hypothetical proteina
3	98.5	7.6	438	2 T45785	DNA-directed RNA p hypothetical proteina
4	97	7.4	1301	2 T07321	DNA-directed RNA p hypothetical proteina
5	93.5	7.2	1489	2 G83771	DNA-directed RNA p hypothetical proteina
6	91	7.0	661	2 T08872	DNA-directed RNA p hypothetical proteina
7	91	7.0	729	1 A36796	kinesin-related protein kinase Drb
8	90.5	6.9	781	1 TVFFDF	hypothetical proteina
9	89.0	6.9	349	2 D70398	hypothetical proteina
10	89.5	6.9	680	2 T04647	hypothetical proteina
11	89.5	6.9	1040	2 AH1926	probable glycoprotein B
12	89	6.8	586	2 JC4778	glycoprotein B (im pectinesterase (EC 3.1.6.1))
13	88.5	6.8	1111	2 T01078	hypothetical proteina
14	87	6.7	1445	2 T50508	hypothetical proteina
15	86	6.6	407	2 F72343	hypothetical proteina
16	86	6.6	830	1 B40407	glycoprotein B
17	86	6.6	830	2 T41186	probable glycoprotein B
18	86	6.6	830	2 T43999	glycoprotein B (im trithorax homolog)
19	85.5	6.6	868	2 T25716	hypothetical proteina
20	85.5	6.6	950	2 T38777	probable valyl tRNA synthetase
21	85.5	6.6	1121	2 T25715	hypothetical proteina
22	85	6.5	930	2 T32017	hypothetical proteina
23	85	6.5	4385	2 T29042	hypothetical proteina
24	84	6.4	3968	2 A44265	trithorax homolog
25	83	6.4	630	2 A49656	estrogen-response element-binding protein
26	83.5	6.4	816	2 D84601	hypothetical proteina
27	83	6.4	287	2 T48548	hypothetical proteina
28	83	6.4	830	1 A44047	glycoprotein B
29	83	6.4	1698	2 S51869	probable membrane

RESULT 1

B38957

interleukin 12A precursor [validated] - human interleukin 12A precursor [validated] - natural killer cell

C;Species: Homo sapiens (man)

C;Date: 18-Aug-1995 #Sequence revision 18-Aug-1995 #Text_change 09-Jul-2004

C;Accession: B38957; A39359; A36055

R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.; i, G.; Perussia, B.

J. Immunol. 146, 3074-3081, 1991

A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric cy

A;Reference number: A38957; MUID:9120875; PMID:1673147

A;Accession: B38957

A;Molecule type: mRNA

A;Residues: 1-253 <NOL>

A;Cross-references: UNIPROT:O6595; GB:M65290

A;Note: it is uncertain whether Met-1 or Met-35 is the initiator R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McCormac, W.; Motyka, R.; Nabav

Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991 A;Title: Coexpression of two distinct genes is required to generate secreted bioactive A;Reference number: A39359; MUID:91239523; PMID:1674604

A;Accession: A39359

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 35-246, T, 248-253 <GUB>

A;Cross-references: GB:M65271; GB:M38443; PID:9180623; PID:9180624

R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.; Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990 A;Title: Purification to homogeneity and partial characterization of cytotoxic lymphocy

A;Reference number: A36055; MUID:90370873; PMID:2204066

A;Accession: A36055

A;Status: preliminary

A;Molecule type: protein

A;Residues: 'X', 58-70, 'X', 72-82 <STE>

C;Genetics: IGD:II12A, NKSP1

A;Cross-references: GDB:127869; OMIM:161560

A;Map position: 3p12.3q13.2
C;Keywords: cytokine, glycoprotein, heterodimer F;57-253/Product: interleukin 12A #status predicted <WAT> F;127,141,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Similarity 100.0% ; Score 1304 ; DB 2 ; Length 253 ; Best Local Similarity 100.0% ; Pred. No. 3_5e-101 ; Mismatches 0 ; Indels 0 ; Gaps 0 ; Matches 253 ; Conservative 0 ;

Qy 1 MWPPGASOPPPSPAAATGHPARPVSLQCRLSMCPARSLVATLVLDDHLSLARNLP 60 Db 1 MWPPGASOPPPSPAAATGHPARPVSLQCRLSMCPARSLVATLVLDDHLSLARNLP 60

Qy 61 VATPDRGMPPOLHKGONLLRAVSNNMLQKAROTLBFYPCTSBEIDHDITDXTSYEACL 120

ALIGNMENTS

61	VATPPGMPPLHHSONILRAVNMQLKARQTEFYCTSEEIDHEDITKDTSVRACL	120
121	PLELTKNESCLNSRETSFITNGSCLASRKTSFPMALCLSSITYELKMYQEFTKTMNAKL	180
121	PLELTKNESCLNSRETSFITNGSCLASRKTSFPMALCLSSITYELKMYQEFTKTMNAKL	180
181	MDPKEQIFLDONMLAVIDELMQLNFNSSETVPQKSSEEEPDTYKTKIKUCILIHAFRIRA	240
181	MDPKEQIFLDONMLAVIDELMQLNFNSSETVPQKSSEEEPDTYKTKIKUCILIHAFRIRA	240
241	VTIDIVMSYLNAS	253
241	VTIDIVMSYLNAS	253

RESULT 2
 56135
 Interleukin 12 p35 subunit - mouse
 Species: Mus musculus (house mouse)
 Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 Accession: I56135
 Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
 Immunol. 148, 3433-3440, 1992
 Title: Cloning and Expression of Murine IL-12.
 Reference number: 156135; MUID:92268481; PMID:1350290
 Accession: I56135
 Status: preliminary; translated from GB/EMBL/DDBJ
 Molecule type: mRNA
 Residues: 1-215 <RES>
 Cross-references: TINTPOD:DA1431; CR:NR6672; NTD:G108316; PTIN:AAA330292 1; PTD:G108317

Query Match	49.4%	Score 644;	DB 2;	Length 215;
Best Local Similarity	58.9%	Pred. No.	2.5e-46	
Matches	129;	Conservative	33;	Mismatches 53; Indels 4; Gaps 1;
35	MCPARSLLVATLVLDLHLSTARLNLPVATPDEGMFPCLAHSSONLRLAVSNMLQKAROTLE	94		
1	MCQSYYLLPLTALLNHLSLARVIPSGP---ARCQSQSNLKLTKTDDMVYKTAEELK	56		
95	FYPCTSEEIDHEDETDKTSTVEAICLPLELTKNECSCLNSRETSFITNGSCLASRKTSFMM	154		
57	HYSCTAEDIDEDETDQTSTLKTCIPLLELHKNECSCLATRETSSTRGSCLPFPQKTSLMM	116		
155	ALCLSSIYEDLKMHQVEFKTNNAKLMDPKQIFLDOMMIAVDEMAQALNENSETYPOK	214		
117	TLCUGSSIYEDLKMHQTEFOALNAALQNNHHQQLIDKGMLVAIDELMQSLNNGETLRQK	176		
215	SSLBBDPFYKIKCILLLAHFRRAVTIDRMSYLNAS	253		
177	PPVGADDPYRVMCLCILLLAHFRRAVTIDRMSYLNAS	215		

Hypothetical protein F26O13.180 - *Arabidopsis thaliana*
 Species: *Arabidopsis thaliana* (mouse-ear cress)
 Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 Accession: T45785
 DeSantis, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
 Submitted to the Protein Sequence Database, December 1999
 Reference number: Z23013

Status: preliminary
 Molecule type: DNA
 Residues: 1-438
 Cross-references: UNIPROT:Q9SCZ5 ; EMBL:AL133452
 Experimental source: cultivar Columbia; BAC clone F26O13
 Genetics:
 ;Map position: 3
 ;Introns: 35/1; 67/2; 104/3; 326/3
 ;Note: F26O13.180
 Query Match 7.6%; Score 98.5%; DB 2; Length 438;

	Best Local Similarity Matches	25.6†;	Pred. No. 1.5;	Mismatches	27;	Indels	48;	Gaps	9;
3	PRGSASDOPPPSSPAATGLHPAARPVSIQCRUSMC	-	-	PARSLLYATLVILDHLSLARN	5.8				
272	PRGRASAPSPLIETFGSQTSHTTTPKS	I	KPSAVADSTRPGRHLRSVASQMANHLDLARN						3.31
59	LPVAT	--	PDGCMFPCLHHQSQNLLRAYSNNMCKARQTLFPECTS	-	-	-	-	-	BBIDH 1.05
332	GRVSTTIFSSPMLYP	--	-HS--IRSSSSGIRK-	-	-	-	-	-	PGSSSGCSSSNHEBDG 3.77
106	EDITDKTSVFACLPYLETONSC	-	-	-LN-	-	-	-	-	SRETSPTN 1.41
378	RSLLTKEGNNTTE	-	-	-	-	-	-	-	-NQGDSARYDALINVKDVEOTNWILN 4.13

RESULT 4
 107321
 cDNA-directed RNA polymerase (EC 2.7.7.6) beta chain - *Chlorella vulgaris* chloroplast
 [Species: *Chlorella vulgaris*]
 [Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
 [Accession: T07321
 [Author: Wakasugi, T.; Kapoor, M.; Sugita, M.; Ito, S.; Taudzuki, J.; Nakamura, Y.]
 [Title: Complete nucleotide sequence of the chloroplast genome from the green alga *Chlorella vulgaris*]
 [Text: Reference number: 215985; PMID: 9159184
 [Accession: T07321
 [Status: preliminary; translated from GB/EMBL/DDJB
 [Molecule type: DNA
 [Producers: J.R.1001 - WAKA]

Sequence analysis results for UniProt ID: Q92221-552, PDB: 3D00, tRNA						
Genetics:		Protein sequence analysis				
Query	Match	Score	Length	DB	Version	Accession
Gene: rpoB	Gene: rpoB	7.44	1301	97	DB 2;	Length 1301;
Chloroplast	Chloroplast	22.48	8	Best Local Similarity	Pred. No. 7-8;	
DNA-directed RNA polymerase beta chain	DNA-directed RNA polymerase beta chain	33	8	Matches	Mismatches	
nucleotidyltransferase	nucleotidyltransferase	54	10	Conservative	Indels	Gaps
chloroplast; chloroplast	chloroplast; chloroplast	92	10			
44 VATLVLDLHSLARNLDPVATPPGMMFCLHSQS-NLLRAVSNMLQKARQTLLE-----	44 VATLVLDLHSLARNLDPVATPPGMMFCLHSQS-NLLRAVSNMLQKARQTLLE-----	94	94			
574 VTRITQSVLQLQNTSVAT--SLPFLERNDANRALMGSMQRQAVPLLPQAPLYGT	574 VTRITQSVLQLQNTSVAT--SLPFLERNDANRALMGSMQRQAVPLLPQAPLYGT	630	630			
95 -FYPCTSEEDIE-----DTIKDKTSTVEACLP-----	95 -FYPCTSEEDIE-----DTIKDKTSTVEACLP-----	130	130			
631 GIESRVIGDVNHSMQAASKTGTPITKVSSSTKIQVLSPRTKAQSFSVSHVLFSLNKRRKGS	631 GIESRVIGDVNHSMQAASKTGTPITKVSSSTKIQVLSPRTKAQSFSVSHVLFSLNKRRKGS	690	690			
131 INSRTEFSITNGSCL-----ASRCTSFWMALCLSSYYEDLKMYQVEFKTNNAKLLMDP	131 INSRTEFSITNGSCL-----ASRCTSFWMALCLSSYYEDLKMYQVEFKTNNAKLLMDP	183	183			
691 LNSEKQFQSKHGIFFIKTLOOKSNNLKNIIFSSA--QKALYOQEINSSFDIKPEAQNRF--LFP	691 LNSEKQFQSKHGIFFIKTLOOKSNNLKNIIFSSA--QKALYOQEINSSFDIKPEAQNRF--LFP	746	746			

RW Human; interleukin 12; IL-12; heterodimeric complex; immunogenic;
Leishmania; antigen; leishmaniasis; cell-mediated immunity; adjuvant;
TH1 helper cell; TH2 helper cell; alum; cytokine; bacterium; cancer;
vaccine; cell surface; membrane; glycoprotein; antigen presenting cell.

RW XX

OS Homo sapiens.

XX PN US5571515-A.

XX DR 05-NOV-1996.

XX PP 17-JUN-1994; 94US-00265087.

XX PR 18-APR-1994; 94US-00229282.

XX PA (WIST) WISTAR INST ANATOMY & BIOLOGY.
(UYFE) UNIV PENNSYLVANIA.

PI Trinchieri G, Scott P;

XX DR WPI; 1996-1505347/50.

XX DR N-PSDB; AAT48098.

PT Immunogenic compn. to improve cell mediated immune response - contains soluble leishmania antigen and interleukin-12 as adjuvant.

XX Disclosure; Col 17-22; 22pp; English.

CC This is the amino acid sequence of the human interleukin (IL)-12 40 kD subunit. IL-12 is a heterodimeric complex composed of the 40 kD subunit and a 30 kD subunit (AAW0739). The complex is used in a novel CC immunogenic composition comprising a soluble Leishmania antigen with IL-12, for protection against leishmaniasis. The addition of IL-12 improves cell-mediated immunity by inducing TH1 helper cells (as opposed to TH2 cells which are induced by alum adjuvant) and does not cause uncontrolled release of other cytokines (in contrast to bacterial adjuvants). IL-12 can also be used as a cancer vaccine by association with the protein B7, a soluble, cell-surface (membrane)-bound glycoprotein which is expressed in antigen presenting cells. (Updated on 25-MAR-2003 to correct PP field.)

XX SQ Sequence 328 AA;

Query Match Score 1758; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1_5e-148;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCHQQLYTISWPSLVLPLASPVAIWELKKDDVVYVLDIYDPDAGEMVTLCDTPBEGITW 60
Db 1 MCHQQLYTISWPSLVLPLASPVAIWELKKDDVVYVLDIYDPDAGEMVTLCDTPBEGITW 60

Qy 61 TLDQSEVLGSGKTLTQKEFGDAQTYCHRGGEVLSHSLLLHKKEKGIVSTDLKDQ 120
Db 61 TLDQSEVLGSGKTLTQKEFGDAQTYCHRGGEVLSHSLLLHKKEKGIVSTDLKDQ 120

Qy 121 KEPKNTPLREAKOYSGRFTCWWLTTISDLTFSVKSRSGSSDPOGVTCGAATLSAERY 180
Db 121 KEPKNTPLREAKOYSGRFTCWWLTTISDLTFSVKSRSGSSDPOGVTCGAATLSAERY 180

Qy 181 RGDNKEYEVSVECDSDACPAAEBSLPIEVMDAVHKLKENYTSFPRDIIKPDPPRN 240
Db 181 RGDNKEYEVSVECDSDACPAAEBSLPIEVMDAVHKLKENYTSFPRDIIKPDPPRN 240

Qy 241 LQLRPLKNRQEVSWEYPTWSPHSYSLTFCVQVQGSKSKEKKDRYVFTDKTSATVIC 300
Db 241 LQLRPLKNRQEVSWEYPTWSPHSYSLTFCVQVQGSKSKEKKDRYVFTDKTSATVIC 300

Qy 301 RKNASISVAQDRYSSSSWSEASVPCs 328
Db 301 RKNASISVAQDRYSSSSWSEASVPCs 328

XX PD 40 kDa subunit of human cytotoxic lymphocyte maturation factor.

XX KW Cytotoxic lymphocyte maturation factor; CLMP; 40 kDa subunit;

XX KW interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;

XX KW CLMP bioactivity inhibition; affinity ligand; transplantation;

XX KW cytotoxic T cell proliferation.

OS Homo sapiens.

XX PN EP790255-A2.

XX PD 20-AUG-1997.

XX PF 09-DEC-1990; 97EP-00104656.

XX PR 22-DEC-1989; 89US-00455708.

PR 09-MAY-1990; 90US-0020935.

PR 27-AUG-1990; 90US-0072284.

PR 09-DEC-1990; 90EP-00123670.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;
Podlanski RJ, Stern AS;

XX DR WPI; 1997-4464698/38.

DR N-FSDB; AAT77849.

XX PT Antibodies to cytotoxic lymphocyte maturation factor protein - useful as affinity ligands, assay reagents and medicaments.

XX PS Claim 2; Fig 25; 80pp; English.

XX The present sequence represents the 40 kDa subunit of cytotoxic lymphocyte maturation factor (CLMP) protein. The natural CLMP protein is a 75 kDa heterodimer, where the 2 subunits (see AAW24236 for the 35 kDa subunit) are bonded together via one or more disulphide bonds. CLMP protein is produced by a human B lymphoblastoid cell line. CLMP synthetically induces in the presence of interleukin-2, the cytolytic activity of lymphokine activated killer cells. CLMP is also capable of stimulating T-cell growth. A novel antibody directed against an epitope of CLMP protein (see AAW24237 for epitope) is capable of neutralising and/or inhibiting CLMP bioactivity. This antibody may be used as an affinity ligand for purifying the CLMP protein. The antibody can also be used as an assay reagent for detecting the CLMP protein, and as a medicament for selectively blocking the proliferation and activation of cytotoxic T cells, e.g. in transplantation, e.g. in transplantation and correct PR field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 328 AA;

Query Match Score 1758; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1_5e-148;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCHQOLVISMSLVLPLASPVAIWELKKDDVVYVLDIYDPDAGEMVTLCDTPBEGITW 60
Db 1 MCHQOLVISMSLVLPLASPVAIWELKKDDVVYVLDIYDPDAGEMVTLCDTPBEGITW 60

Qy 61 TLDQSEVLGSGKTLTQKEFGDAQTYCHRGGEVLSHSLLLHKKEKGIVSTDLKDQ 120
Db 61 TLDQSEVLGSGKTLTQKEFGDAQTYCHRGGEVLSHSLLLHKKEKGIVSTDLKDQ 120

Qy 121 KEPKNTPLREAKOYSGRFTCWWLTTISDLTFSVKSRSGSSDPOGVTCGAATLSAERY 180
Db 121 KEPKNTPLREAKOYSGRFTCWWLTTISDLTFSVKSRSGSSDPOGVTCGAATLSAERY 180

Qy 181 RGDNKEYEVSVECDSDACPAAEBSLPIEVMDAVHKLKENYTSFPRDIIKPDPPRN 240
Db 181 RGDNKEYEVSVECDSDACPAAEBSLPIEVMDAVHKLKENYTSFPRDIIKPDPPRN 240

Qy 241 LQLRPLKNRQEVSWEYPTWSPHSYSLTFCVQVQGSKSKEKKDRYVFTDKTSATVIC 300
Db 241 LQLRPLKNRQEVSWEYPTWSPHSYSLTFCVQVQGSKSKEKKDRYVFTDKTSATVIC 300

Qy 301 RKNASISVAQDRYSSSSWSEASVPCs 328
Db 301 RKNASISVAQDRYSSSSWSEASVPCs 328

Qy 121 KEPKNTPLREAKOYSGRFTCWWLTTISDLTFSVKSRSGSSDPOGVTCGAATLSAERY 180

GenCore version 5.1.6
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Run on: December 26, 2004, 09:32:55 ; Search time 437.322 Seconds
 (without alignments)
 15189.855 Million cell updates/sec

OM nucleic - nucleic search, using sw model

Title: US-10-655-873-11
 Perfect score: 1193
 Sequence: 1 tgaatcgtatgtaaagttaaatgttccaaact 1193

Scoring table: IDENTITY_NUC
 Gapext 1.0 , Gapext 1.0
 Searched: 4105333 seqs, 278495677 residues
 Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:
 1: /cgn2_6/prodata/1/pubpna/JS07_PUBCOMB.seq:
 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
 3: /cgn2_6/prodata/1/pubpna/US05_NEWPUB.seq:
 4: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 5: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 6: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 7: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 8: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 9: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 10: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 11: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 12: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 13: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 14: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 15: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 16: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
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 22: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
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 25: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 26: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 27: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 28: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
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 34: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 35: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 36: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 c: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 37: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 38: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 c: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 39: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 c: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 40: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 c: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 41: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 c: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 42: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 c: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 43: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 44: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:
 45: /cgn2_6/prodata/1/pubpna/US05_PUB.seq:

ALIGNMENTS

RESULT 1
US-10-284-740-13
Sequence 13, Application US/10284740
Publication No. US2013038404A1
GENERAL INFORMATION:
APPLICANT: Maroun, Leonard E.
TITLE OF INVENTION: INTERFERON ANTAGONISTS USEFUL FOR THE TREATMENT OF INTERFERON RELATED DISEASES
FILE REFERENCE: 18448/2002
CURRENT APPLICATION NUMBER: US/10/284,740
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 09/845,260
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 09/067,398
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: US 08/502,519
PRIOR FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (109)..(609)
OTHER INFORMATION:
US-10-284-740-13

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Query Match      100.0%; Score 1193; DB 15; Length 1193;
Best Local Similarity 100.0%; Prid. No. 2.6e-244;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy 1 TGAAGTCAGGCTATTAGAAGAGAAAGATCAGTTAAGTCCTTGACCTGATCAGCTGTAT 60

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SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	1193	100.0	1193	15	US-1-254-740-13	Sequence 13, Appl
2	1193	100.0	1193	16	US-10-641-643-1302	Sequence 1302, Ap
3	1193	100.0	1193	17	US-10-283-975A-258	Sequence 258, App
4	1193	100.0	1193	17	US-10-654-796-6	Sequence 6, Appl
5	1193	100.0	1193	17	US-10-654-763-6	Sequence 6, Appl
6	1193	100.0	1193	18	US-10-733-878-280	Sequence 280, App
7	963.2	80.7	987	10	US-0-982-945A-141	Sequence 141, App
8	963.2	80.7	987	18	US-10-807-114-141	Sequence 141, App
9	718.8	60.3	5961	15	US-10-129-802-35	Sequence 35, Appl
10	718.8	60.3	5961	16	US-10-330-503-26	Sequence 26, Appl
11	501.8	42.1	601	15	US-10-267-384-168	Sequence 168, App
12	419.4	41.9	501	16	US-10-411-037-19	Sequence 19, Appl

1 TGAAGATCAGCTATTAGAAAGAAAGATCAGTTAAGTCAGCTTGGACCTGATCAGCTTGAT 60
 61 ACAAGAACTACTGATTCAACTCTTGGCTTAATCTCAGGAAACGATGAAATAACA 120
 61 ACAGAACTACTGATTCAACTCTTGGCTTAATCTCAGGAAACGATGAAATAACA 120
 121 AGTTATCATCGCTTTCACTCTGCATCTTGGCTTAATCTCAGGAAACGATGAAATAACA 180
 121 AGTTATCATCGCTTTCACTCTGCATCTTGGCTTAATCTCAGGAAACGATGAAATAACA 180
 181 GACCCTATGTAAGAGGAAACCTTAGAATATTAAATGAGCTCATTCAGAT 240
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 241 GTAGCGATTAATGGAACTCTTCAGGATTGAAAGGAGGTGAC 300
 241 GTAGCGATTAATGGAACTCTTCAGGATTGAAAGGAGGTGAC 300
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 361 GATGACCAAGGCATCCAAAAGAGTGTGGAGAACCATCAAGGAGACATGATGTCAGATT 420
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 421 TTCAATAGCAACAAAAGAACGAGATGACTCTGGAAAGGTGACTAAATTTCGTTGAACT 480
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 961 CAGTTACTGGGTTGAAATAATGCTGAACTGTTTAATGGCATGTC 1020
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 181 GACCCATATGTAAGAGGAAACCTTAAGAAATTTAAATGCACTTCAAGAT 1140
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Qy 1141 TGTTAAATTATCTAATATCTAATATGAAATAAGTAAAGTAAAGTTCAGACT 1193
 Db 1141 TGTTAAATTATCTAATATCTAATATGAAATAAGTAAAGTAAAGTTCAGACT 1193
 ; Sequence 1302, Application US/10641643
 ; Publication No. US2004007703A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocke, Benjamin G.
 ; Susan G. Stuart
 ; Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/641,643
 ; FILING DATE: 14-Aug-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: <Unknown>
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1302:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1193 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: 932691
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1302 :
 US-10-641-643-1302

Query Match 100.0%; Score 1193; DB 16; Length 1193;
 Best Local Similarity 100.0%; Pred. No. 2,68-244;
 Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 ACAGAACTACTGATTCAACTCTTGGCTTAATTCTCTCGAAACGATGAAATAACA 120
 Qy 1 TGAGATCAGCTATTAGAGAGAAAGTCACTTGTGACTTGTGACTTGTGAT 60
 Db 61 ACAGAACTACTGATTCAACTCTTGGCTTAATTCTCTCGAAACGATGAAATAACA 120
 Qy 121 AGTTATCTGGCTTCAACTGTTGACTGTCAGCTGATGAAATTTGCTGTTACTGCCAG 180
 Db 121 AGTTATCTGGCTTCAACTGTTGACTGTCAGCTGATGAAATTTGCTGTTACTGCCAG 180
 Qy 181 GACCCATATGTAAGAGGAAACCTTAAGAAATTTAAATGCACTTCAAGAT 240
 ; Sequence 1302, Application US/10641643
 ; Publication No. US2004007703A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocke, Benjamin G.
 ; Susan G. Stuart
 ; Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/641,643
 ; FILING DATE: 14-Aug-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: <Unknown>
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1302:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1193 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: 932691
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1302 :
 US-10-641-643-1302

Query Match 100.0%; Score 1193; DB 16; Length 1193;
 Best Local Similarity 100.0%; Pred. No. 2,68-244;
 Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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 SOM protein - protein search, using sw model
 Run on: December 26, 2004, 10:00:30 ; Search time 31.5556 seconds
 (without alignments)
 1887.118 Million cell updates/sec

 title: US-10-655-873-12
 Perfect score: 856
 Sequence: 1 MKTYSTYLLAFQLCIVLGLSGL.....AKTOKRKRSQMLFGGRASSQ 166

 Scoring table: BloSUM62
 Gapop 10.0 , Gapext 0.5

 Searched: 2002273 seqs , 35872999 residues

 Total number of hits satisfying chosen parameters: 2002273

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minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

database : A_GenSeq_23Sep04:*
1: geneseqD1980s;*
2: geneseqD1990s;*
3: geneseqD2000s;*
4: geneseqD2001s;*
5: geneseqD2002s;*
6: geneseqD2003as;*
7: geneseqD2003bs;*

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No greater is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the record.

סְבִירָה

Result No.	Score	% Summary			Description	
		Query	Match	Length	DB ID	
1	856	100.0	166	1	AAP9414	Aap9314 INF211 ,
2	856	100.0	166	7	ADF75401	Adf76401 Novel hum
3	856	100.0	166	7	ADM11723	Adm13723 Human int
4	856	100.0	166	8	ADP1492	Adp1492 Protein e
5	856	100.0	166	8	ADO19766	Ado19766 Human PRO
6	856	100.0	166	8	ADQ09094	Adq09094 Human che
7	852	99.5	166	1	AAP30939	Aap30939 Sequence
8	852	99.5	166	1	AAP40122	Aap40122 Sequence
9	852	99.5	166	1	AAP40153	Aap40153 Sequence
10	852	99.5	166	1	AAP40157	Aap40157 Sequence
11	852	99.5	166	1	AAP50233	Aap50233 Human rec
12	852	99.5	166	2	Aaw70582	Aaw70582 Human int
13	852	99.5	166	4	AAB99130	Aab99130 Human int
14	852	99.5	166	5	AAE15823	Aae15823 Human int
15	852	99.5	166	5	AAU78100	Aau78100 Human int
16	852	99.5	166	5	AAU96670	Aau96670 Human int
17	852	99.5	166	5	ABB07440	Abb07440 Interfero
18	852	99.5	166	6	ABR55848	Abr55848 Human int
19	852	99.5	166	6	ABR40017	Abr40017 Human wil
20	852	99.5	166	6	ABP56461	Abp56461 Human int
21	852	99.5	166	6	ADA94887	Ada94887 Human int
22	852	99.5	166	7	ADC78909	Adc78909 Human int
23	852	99.5	166	8	ADG45031	Adg45031 Human int
24	852	99.5	166	8	ADJ6129	Adj6129 Human int
25	852	99.5	166	8	ADT75952	Adt75952 Human int

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Query Match      100.0%; Score 856; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-77;
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Y 1 MKYTYSIYLAFOLCIVYGSLGXCOPDPYVKBAENLKYCFNAGHSVDADNGTYFTGTTKWKW 60

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28

Db	1	MKTYSTIYLAFLQLCTVLSIGCYCOPYTKAEENKKYFNAGHSVAONGTLFLGILKNWK	60	CC	Invention.	
Qy	61	EBSDRKIMQSQTISFYFLKFKNPFDQSIQKSVENTIEDMNVKPFNSNKKRDDFEKLTN	120	SQ	Sequence 166 AA;	
Db	61	EBSDRKIMQSQTISFYFLKFKNPFDQSIQKSVENTIEDMNVKPFNSNKKRDDFEKLTN	120	Query Match	100.0%; Score 856; DB 7; Length 166;	
Qy	121	YSVTDLNVRKAHELQMAELSPAAKTGKRKRSSQMLFQGRRASQ	166	Best Local Similarity	100.0%; Pred. No. 2e-77; 0; Mismatches 0; Gaps 0;	
Db	121	YSVTDLNVRKAHELQMAELSPAAKTGKRKRSSQMLFQGRRASQ	166	Matches 166; Conservative	0; Mismatches 0; Gaps 0;	
RESULT 2				Qy	1 MKCTSYLIAFLQCIULGSLLGCYCQDPVKEAENKKYFNAGHSVAONGTLFLGILKNWK	60
ID	ADF76401	standard; protein; 166 AA..		Db	1 MKCTSYLIAFLQCIULGSLLGCYCQDPVKEAENKKYFNAGHSVAONGTLFLGILKNWK	60
XX				Qy	61 EBSDRKIMQSQTISFYFLKFKNPFDQSIQKSVENTIEDMNVKPFNSNKKRDDFEKLTN	120
AC	ADF76401;			Db	61 EBSDRKIMQSQTISFYFLKFKNPFDQSIQKSVENTIEDMNVKPFNSNKKRDDFEKLTN	120
XX				Qy	121 YSVTDLNVRKAHELQMAELSPAAKTGKRKRSSQMLFQGRRASQ	166
DT	26-FEB-2004	(first entry)		Db	121 YSVTDLNVRKAHELQMAELSPAAKTGKRKRSSQMLFQGRRASQ	166
XX				DE	Novel human secreted and transmembrane protein SeqID 74.	
XX				RESULT 3		
KW	human; PRO; membrane bound protein; membrane bound receptor;			ADM13723		
KW	cell proliferation; cell migration; cell differentiation;			ID	ADM13723 standard; protein; 166 AA.	
KW	mitogenic factor; survival factor; cytokine factor;			XX		
KW	differentiation factor; neuropeptide; hormone; cell receptor;			AC	ADM13723;	
KW	receptor-ligand interaction; cytosstatic; chondrocyte; tumour.			XX		
XX	Homo sapiens.			DT	20-MAY-2004 (first entry)	
OS				XX	Human interferon-gamma protein.	
XX				XX		
PN	WO2003072035-A2.			XX	Interferon, IFN; Alzheimer's disease; Down syndrome; infant encephalitis;	
XX				XX	AIDS-associated dementia; lupus erythematosus;	
PD	04-SEP-2003.			XX	autoimmune disease; HIV; AIDS-associated lateral sclerosis;	
XX				XX	ulcerative colitis; Hashimoto's disease; amyotrophic lateral sclerosis;	
PP	21-FEB-2003; 2003WO-US005241.			XX	Goodpasture's syndrome; therapy; acquired immunodeficiency syndrome;	
XX				XX	AIDS; human.	
PR	22-FEB-2002; 2002US-0359461P.			XX	Homo sapiens.	
XX				OS		
PA	(GETH) GENENTECH INC.			XX		
XX				PN	US2003138404-A1.	
PI	Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;			XX		
PI	Williams PM, Wood WI, Wu TD;			BD	24-JUL-2003.	
XX				XX		
DR	WPI: 2003-721702/68.			PP	31-OCT-2002; 2002US-00284740.	
XX				XX		
DR	N-PSDB; ADF76400.			PR	14-JUL-1995; 95US-00502519.	
XX				PR	28-APR-1998; 98US-0067398.	
PT	New PRO polypeptides, useful for diagnosing and treating an immune			PR	30-APR-2001; 2001US-00845260.	
PT	related disorder, e.g. systemic lupus erythematosus, rheumatoid			XX		
PT	arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or			PA	(MEIO-) MBIODGEN BIOTECHNOLOGY CORP.	
PT	diabetes mellitus.			XX		
PS	Claim 10; SEQ ID NO 74; 918pp; English.			PI	Maroun LE;	
XX				XX		
CC	This invention relates to novel nucleic acids encoding human PRO secreted			DR	WPI; 2003-829690/77.	
CC	and transmembrane proteins. Extracellular proteins play important roles			DR	N-PSDB; ADM13724.	
CC	in the formation, differentiation and maintenance of multicellular			DR	GENBANK; X13274.	
CC	organisms. The fate of many individual cells (for example proliferation,			XX		
CC	migration or differentiation) is typically governed by information			XX	Composition for preventing or decreasing pathological effects of disease	
CC	received from other cells and the immediate environment. The information			PT	that are associated with increased level of or heightened responsiveness	
CC	is often transmitted by secreted polypeptides (for example mitogenic			PT	to interferon, comprises at least two isolated interferon binding	
CC	factors, survival factors, cytotoxic factors, differentiation factors,			XX	proteins.	
CC	neuropeptides and hormones) which are received and interpreted by diverse			XX		
CC	cell receptors or membrane bound proteins. These membrane bound proteins			PS	Disclosure; Fig 7B; 38pp; English.	
CC	and receptors may be of use as pharmaceutical and diagnostic agents, such			XX		
CC	as in the blocking of receptor-ligand interactions. The current invention			CC	The present invention provides composition for preventing or decreasing	
CC	provides the amino acid sequences of novel human membrane bound receptors			CC	pathological effects of a disease that are associated with an increased	
CC	and proteins, along with the cDNA sequences encoding them. The novel			CC	level of or a heightened responsiveness to interferon (IFN) where the	
CC	proteins of the invention may have cytostatic activities through the			CC	composition inhibits the activity of one or more IFN. The invention is	
CC	stimulation of chondrocytes. The nucleic acids of the invention may be			CC	useful for treating diseases such as Alzheimer's disease, Down syndrome,	
CC	useful for the manufacture of a medicament for diagnosing or treating a			CC	infant encephalitis, autoimmune diseases such as lupus erythematosus,	
CC	tumour in a mammal. In addition, they may be useful for measuring or			CC	ulcerative colitis, Hashimoto's disease, amyotrophic lateral sclerosis,	
CC	detecting the expression of a tumour associated gene. The present			CC	and Goodpasture's syndrome, HIV where the administration of the	
CC	sequence is the amino acid sequence of a human PRO protein of the			CC	agonist prevents or ameliorates AIDS (acquired immunodeficiency	